AMENDMENTS TO THE CLAIMS

1-20. (Cancelled)

21. (New) A method for guiding the application of an adjuvant therapy in treating a human patient having a neoplasia, comprising:

a) determining a nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations;

c) classifying the patient into a survival subgroup depending on

(i) the presence or absence of a mutation, and

(ii) whether the patient is node positive or node negative,

wherein the survival rate following the adjuvant therapy of node negative patients without a mutation in p53 is not statistically significant, whereas the survival rate following the adjuvant therapy of node negative patients having a mutation in p53 is significantly improved, and

the survival rate following the adjuvant therapy of node positive patients without a mutation in p53 is not statistically significant, whereas the survival rate following the adjuvant therapy of node positive patients having a mutation in p53 is significantly improved;

d) applying the adjuvant therapy to the patient if the survival rate according to part c) following the adjuvant therapy is significantly improved.

22. (New) A method for determining a prognosis of a human patient having a neoplasia, comprising:

a) determining a nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations;

c) classifying the neoplasia into different subgroups depending on the position of a mutation,

wherein a mutation in conserved region II or conserved region V of p53 is indicative of poor patient outcome in comparison with a mutation outside the conserved regions I-V of p53, and

wherein a mutation in ~~a~~ conserved region III or conserved region IV is indicative of positive patient outcome in comparison with a mutation outside the conserved regions I-V of p53; and

d) determining the prognosis of the patient based on the classification of the neoplasia as determined in part c).

23. (New) A method for guiding the application of an adjuvant therapy in treating a human patient having a neoplasia, comprising:

a) determining a nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on the position of a mutation,

wherein a mutation in conserved region II or conserved region V of p53 is indicative of poor patient outcome in comparison with a mutation outside the conserved regions I-V of p53, and

wherein a mutation in conserved region III or conserved region IV is indicative of positive patient outcome in comparison with a mutation outside the conserved regions I-V of p53; and

d) applying the adjuvant therapy to the patient if the mutation is found in conserved region III or conserved region IV.

24. (New) The method according to claim 21, wherein an exon or exons of the sequenced nucleic acid encode a DNA binding domain.

25. (New) The method according to claim 21, wherein evolutionary conserved regions of the nucleic acid are analyzed.

26. (New) The method according to claim 21, wherein the neoplasia is a breast, lung, prostate, gastric, colorectal or melanoma neoplasia.

27. (New) The method according to claim 22 or 23 wherein the neoplasia is a breast, lung, prostate, gastric, leukemia, colorectal or melanoma neoplasia.

28. (New) The method of claim 26, wherein said neoplasia originates from a breast neoplasia.

29. (New) The method of claim 27, wherein said neoplasia originates from a breast neoplasia.

30. (New) The method according to claim 21, wherein the adjuvant therapy is radiation or chemotherapy/hormone therapy.

31. (New) The method according to any one of claims 21-23, wherein step a) is carried out using an automated nucleic acid sequencer, computer software optionally being used to track samples and control process steps and/or to aid in and/or interpret sequence data obtained.

32. (New) The method according to claim 22 or 23, further comprising the step of typing the mutation of step c) as a missense mutation, a nonsense mutation, a deletion, or an insertion.

33. (New) The method according to claim 32, wherein a frameshift or nonsense mutation in a conserved region II and/or conserved region V of p53 is indicative of poor patient outcome in comparison with a mutation outside the conserved regions I-V of p53.

34. (New) The method according to claim 32, wherein a missense mutation in a conserved region III and/or conserved region IV is indicative of positive patient outcome in comparison with a mutation outside the conserved regions I-V of p53.

35. (New) The method according to claim 32, wherein the following p53 mutations in a node negative patient are indicative of poor patient outcome:

a Glu→Ala substitution at amino acid position 28;

an Ala→Val substitution at amino acid position 159;

a 9 base pair deletion at amino acid position 177;

a His→Gln substitution at amino acid position 179;

an Arg→His substitution at amino acid position 181;

a nonsense mutation at amino acid position 213;

a Cys→Phe substitution at amino acid position 238;

a Met→Thr substitution at amino acid position 246;

an Arg→Ser substitution at amino acid position 249;

a 9 base pair deletion at amino acid position 267;

an Arg→Gly substitution at amino acid position 280; and

a 2 base pair insertion at amino acid position 340.

36. (New) The method according to claim 32, wherein the following p53 mutations in a node positive patient are indicative of poor patient outcome:

a Pro→Leu substitution at amino acid position 36;

a 200 base pair deletion at amino acid position 120;

a 21 base pair deletion at amino acid position 126;

a nonsense mutation at amino acid position 204;

a Tyr→Cys substitution at amino acid position 205;

a 2 base pair deletion at amino acid position 214;

a His→Arg substitution at amino acid position 214;

a Tyr→Cys substitution at amino acid position 220;

a Met→Ile substitution at amino acid position 237;

an Arg→Gln substitution at amino acid position 248;

an Arg→Trp substitution at amino acid position 248;

a 3 base pair deletion at amino acid position 264;

an Arg→Cys substitution at amino acid position 273;

an Ala→Gly substitution at amino acid position 276;

an Arg→Pro substitution at amino acid position 282;

a Glu→Lys substitution at amino acid position 285; and

a 1 base pair insertion at amino acid position 317.